

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 137505

TO: Patricia Duffy

Location: REM/3B05/3C18

Art Unit: 1645

Monday, November 15, 2004

Case Serial Number: 09/765271

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

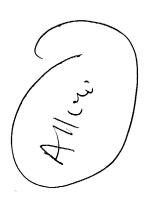
Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527





STIC-Biotech/ChemLib

137505

From:

Duffy, Patricia

Sent:

Tuesday, November 09, 2004 3:48 PM

To:

STIC-Biotech/ChemLib

Subject:

Quick comparison search of proteins.

Importance:

High

IN re:09/765,271

Please run a comparison sequence search comparing SEQ ID NO:56 of 09/765,271 with Accession Number P91742 of SPTREMBL. I need the full length of p19742 compared. I am looking for a short region that has 8 consecutive amino acids in common with SEQ ID NO:56.

Thank you.

Patricia A. Duffy, Ph.D. Art Unit 1645, Remsen 3B05 571-272-0855

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked up:
Date Completed: _____//5
Searcher Prep/Rev. Time:
Online Time:

Type of Search

NA Sequence: #______

AA Sequence : #______

Structure: #______

Bibliographic:______

Litigation:______

Patent Family:_______

Other:

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

November 15, 2004, 16:56:34; Search time 0.001 Seconds (without alignments) 122:584 Million cell updates/sec Run on:

us-09-765-271-56

4165 1 SYELGLYQARTVKENNRVSY.....KLLALLKGSNPSSVSKEKIN 796 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1 segs, 154 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

p91742.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TOIG of: p91742 Description 154 1 p91742 ΩĪ Query Score Match Length DB 7.3 52.5 Result No.

ALIGNMENTS

```
Robertson H.M.;
Robertson H.M.;
Robertson H.M.;
"Multiple Mariner transposons in flatworms and hydras are related to those of insects.";
J. Hered. 88:195-201(1997).
EMBL; US1185; AAB61389:1; -.
IncerPro; IPR001888; Transposase_1.
Pfam; PF01359; Transposase_1; 1.
NON TER 154 154
                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Transposase (Fragment).
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                         PRT; 154 A.A.
                             from: 1 to: 154
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TRANSPOSON=mariner;
MEDLINE=97327060; PubMed=9183847;
                            TOIG of: p91742 check: 1859
                                                         PRELIMINARY;
RESULT 1
```

```
3,
                                                                                                                                            Gaps
                                      P91742 Length: 154 November 15, 2004 16:52 Type: P Check: 1859
                                                                                                                                            7;
                                                                                                    Length 154;
                                                                                                Query Match 1.3%; Score 52.5; DB 1; Length 1 Best Local Similarity 42.1%; Pred. No. 0; Matches 16; Conservative 5; Mismatches 10; Indels
154 AA; 18179 MW; 955FB7091F434F57 CRC64;
                                                                                                                                                                          449 EAHKALFXN---KGR--NSDFQALDKLLERLNDESTNK 481
                                                                                                                                                                                                          Search completed: November 15, 2004, 16:56:34 Job time: 0.001 secs
SEQUENCE
                                                         p91742
                                                                                                                                                                                     à
                                                                                                                                                                                                                       g
```